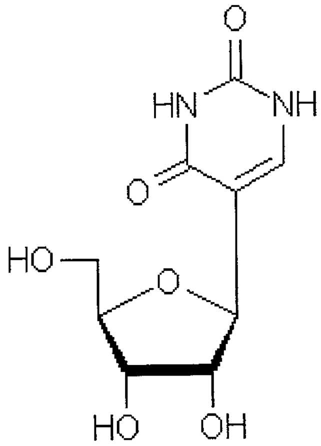
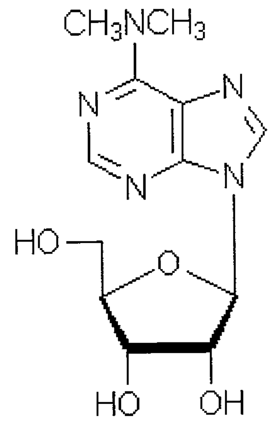
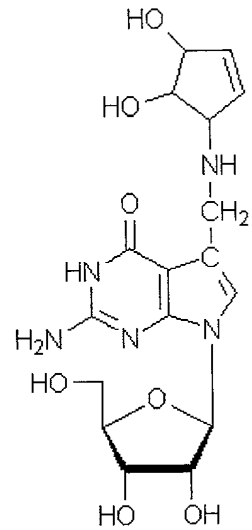
FIGURE 1



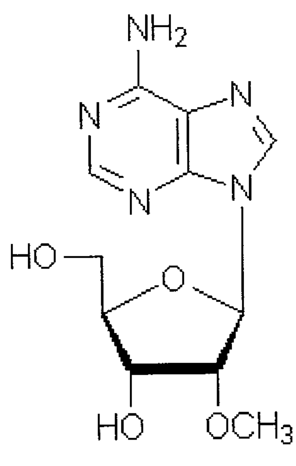
Pseudouridine(Ψ)



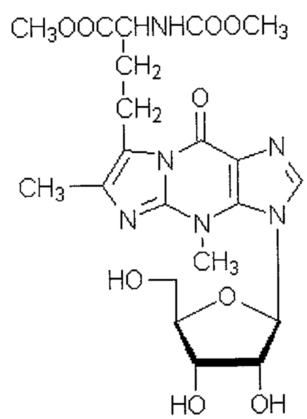
N6,N6-dimethyladenosine



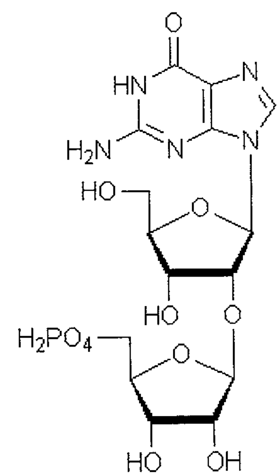
Queuosine(Q)



2'-O-methyladenosine



Wybutosine(yW)



2'-O-ribosylguanosine (phosphate)

FIGURE 2

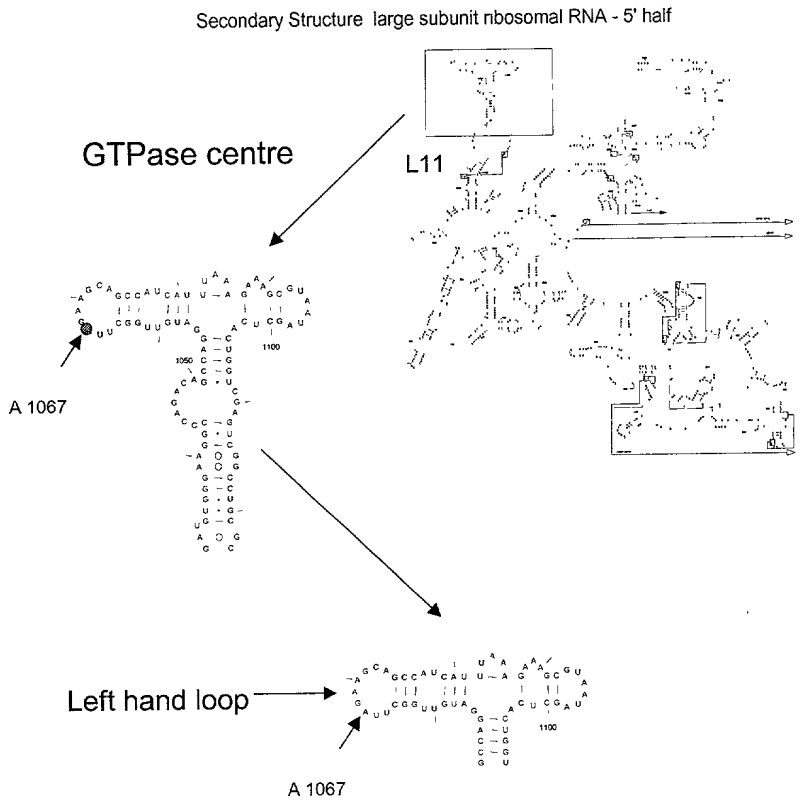


FIGURE 3

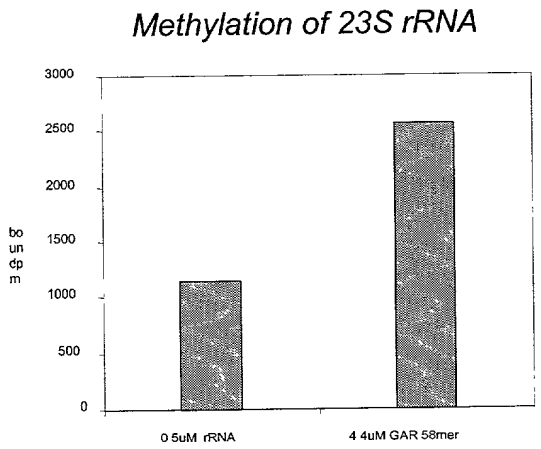


FIGURE 4A

Accessibility of the components of the GAR

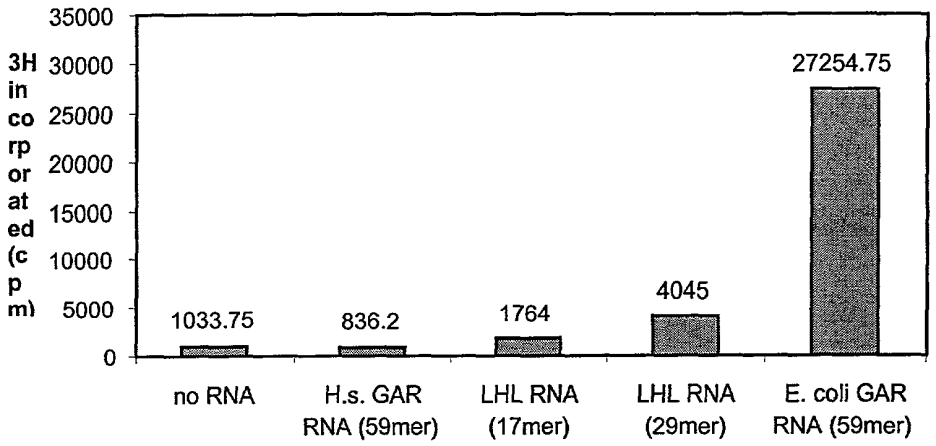


FIGURE 4B

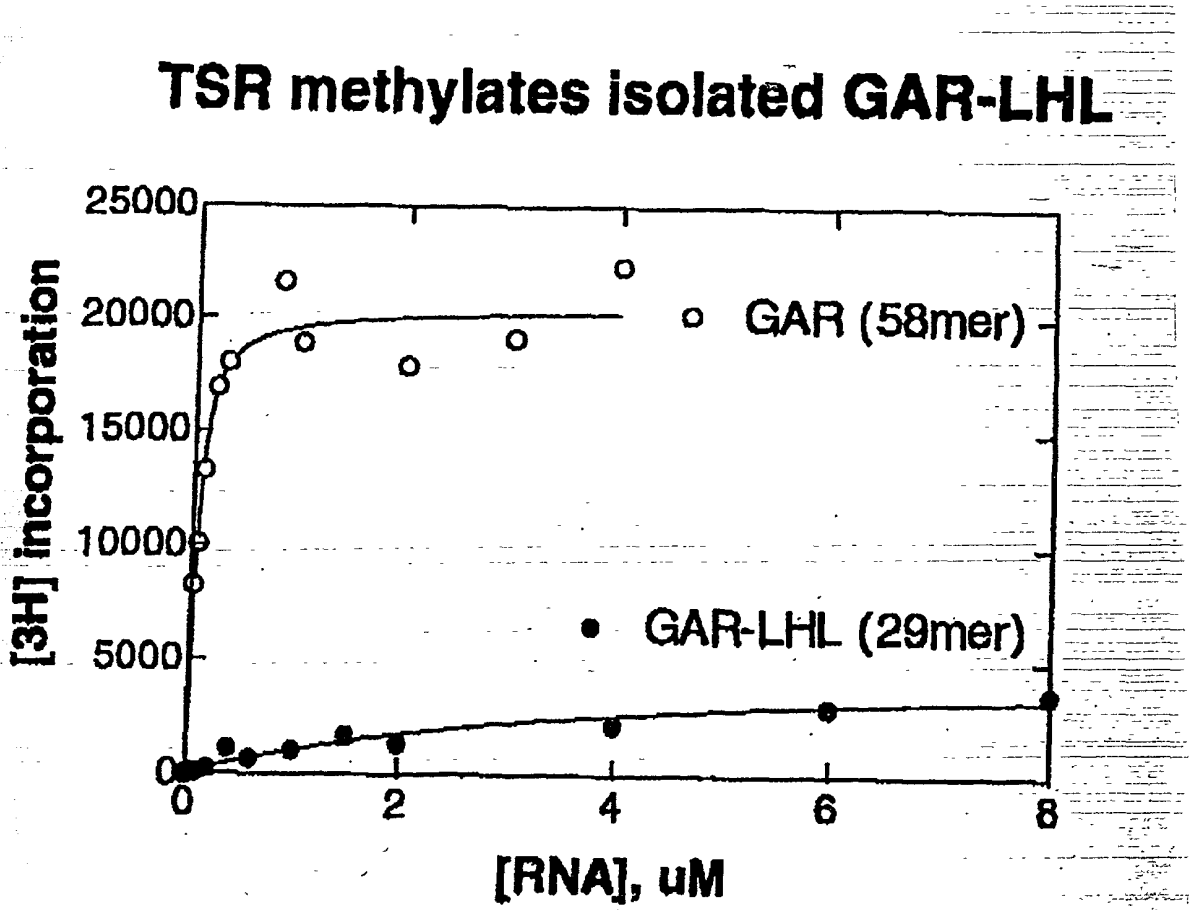


FIGURE 5

Binding of L11 by inhibition of methylation

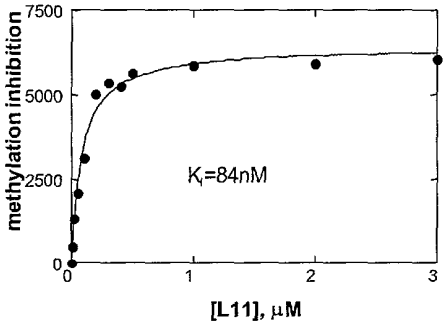


Figure 5

FIGURE 6

Binding of thiostrepton by inhibition of methylation

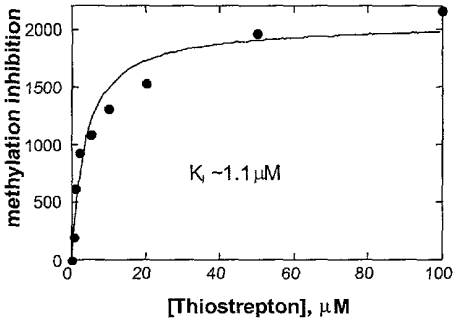


FIGURE 7

Inhibition of TSR methylation by RBT compounds

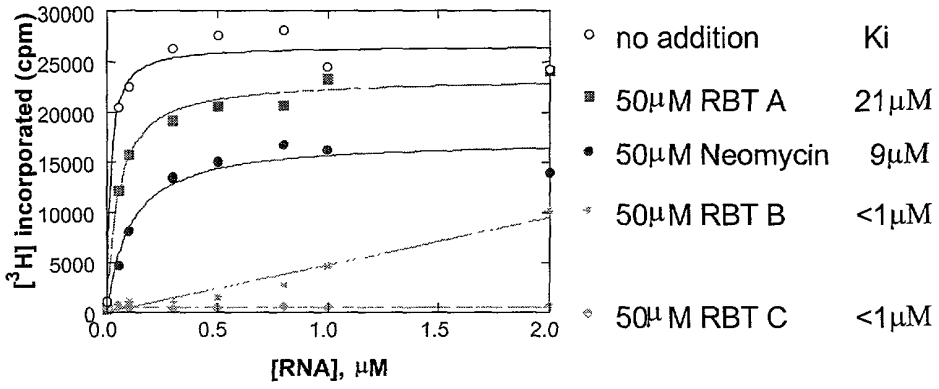
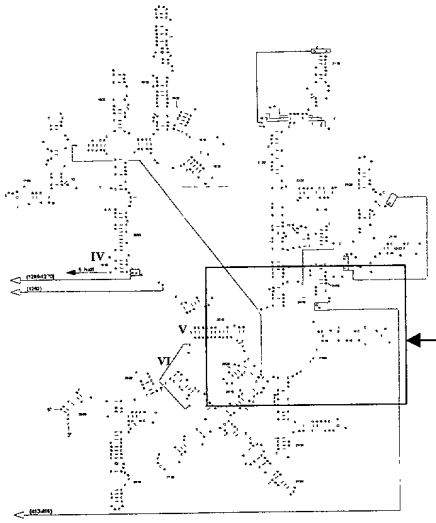
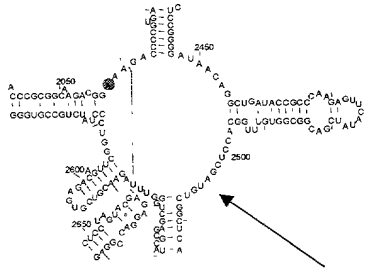


FIGURE 8

Erythromycin resistance methyltransferase (erm)



large subunit ribosomal RNA - 3' half



Peptidyl transferase centre

Figure 8

Peptidyl transferase centre

Erythromycin resistance methyltransferase (erm), dimethylates N6 of A2058 of 23S rRNA.

FIGURE 9

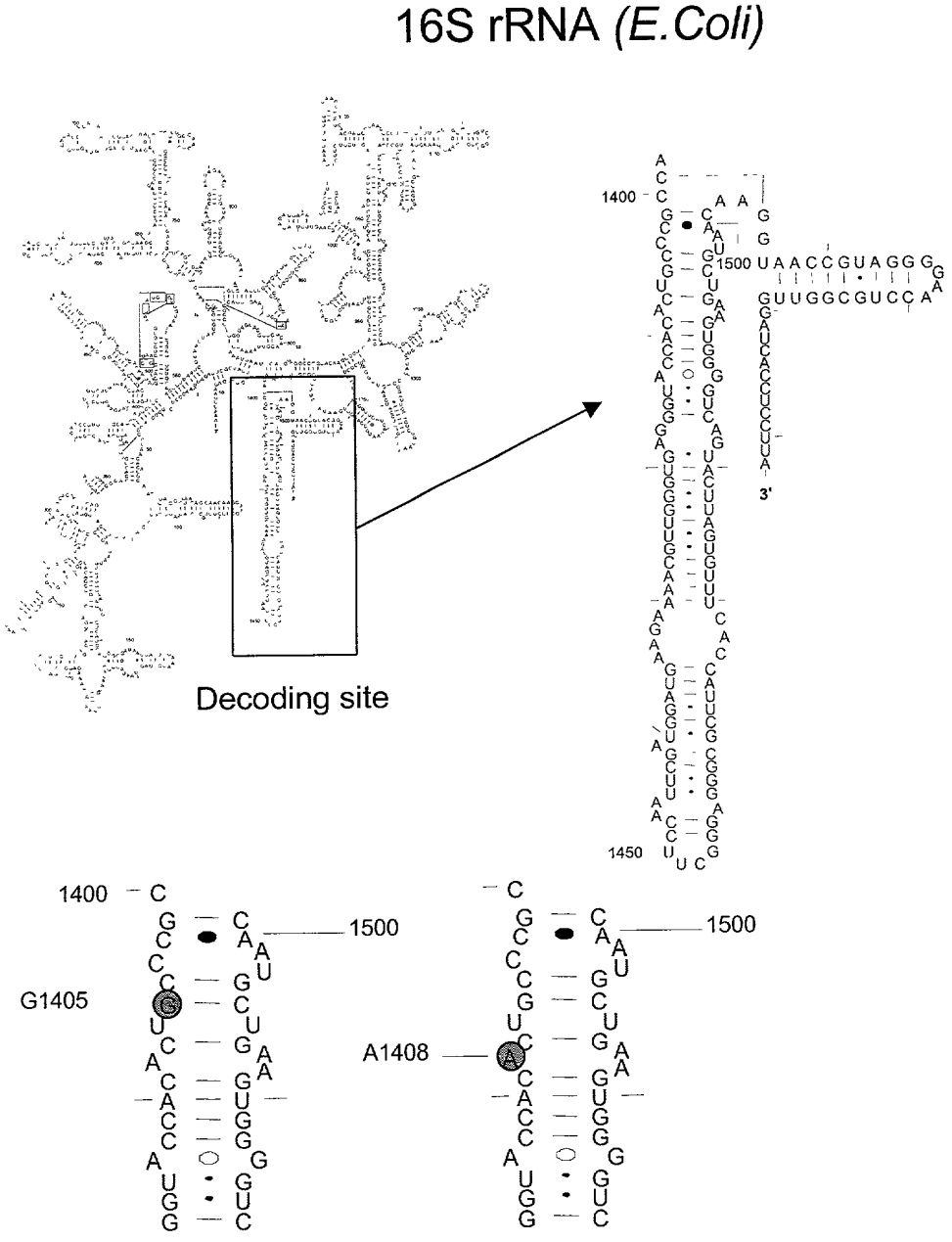


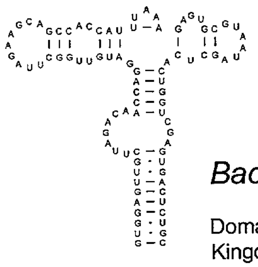
Figure 9

Methylation modifications in the decoding site of 16S rRNA that confer resistance to aminoglycoside antibiotics:

Methyltransferase converts G1405 to 7-methylguanosine
Methyltransferase converts A1408 to 1-methyladenosine

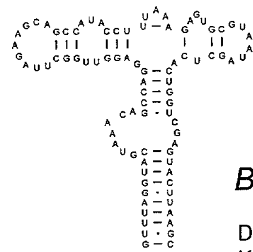
FIGURE 10

Secondary Structure: large subunit ribosomal RNA - 5' half



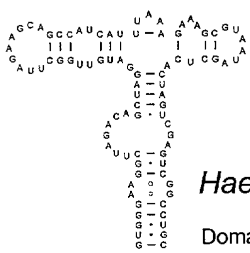
Bacillus subtilis

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Low G+C*



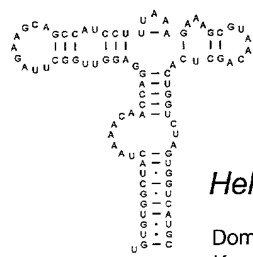
Borrelia burgdorferi

Domain: *Bacteria*
Kingdom: *Spirochaetes*



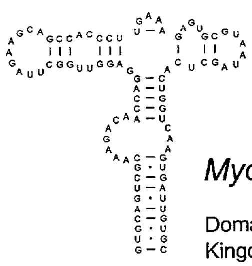
Haemophilus influenzae

Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *gamma*



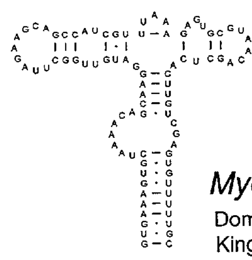
Helicobacter pylori

Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *epsilon ?*



Mycobacterium leprae

Domain: *Bacteria*
Kingdom: *Gram-positve*
Order: *High G+C*



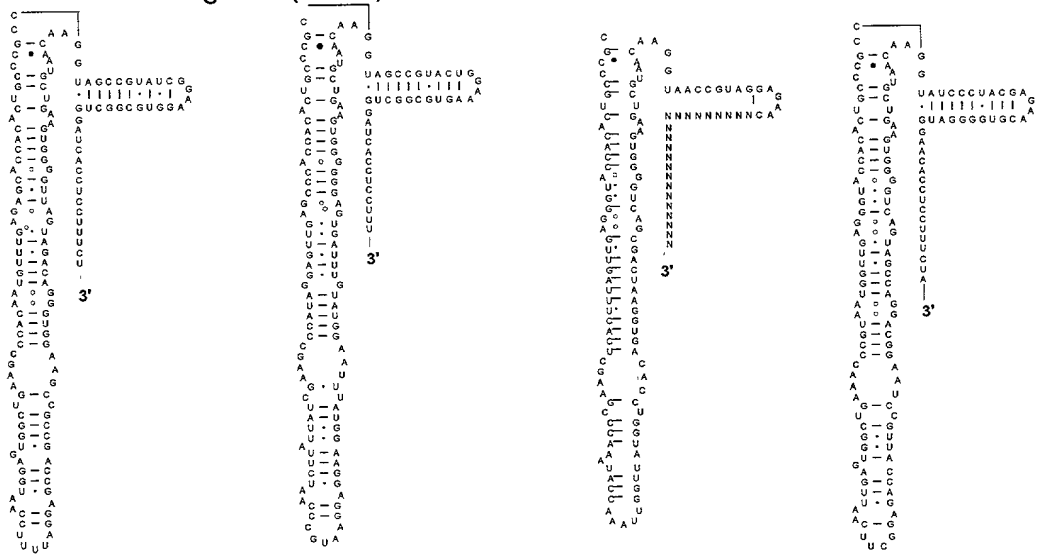
Mycoplasma genitalium

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmales*

Fig10
Sites accessible to the thiostrepton resistance methyltransferase
In a range of bacteria

FIGURE 11

Secondary Structure: small subunit ribosomal RNA:
Decoding Site (A site)



Bacillus subtilis

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Low G+C*

Borrelia burgdorferi

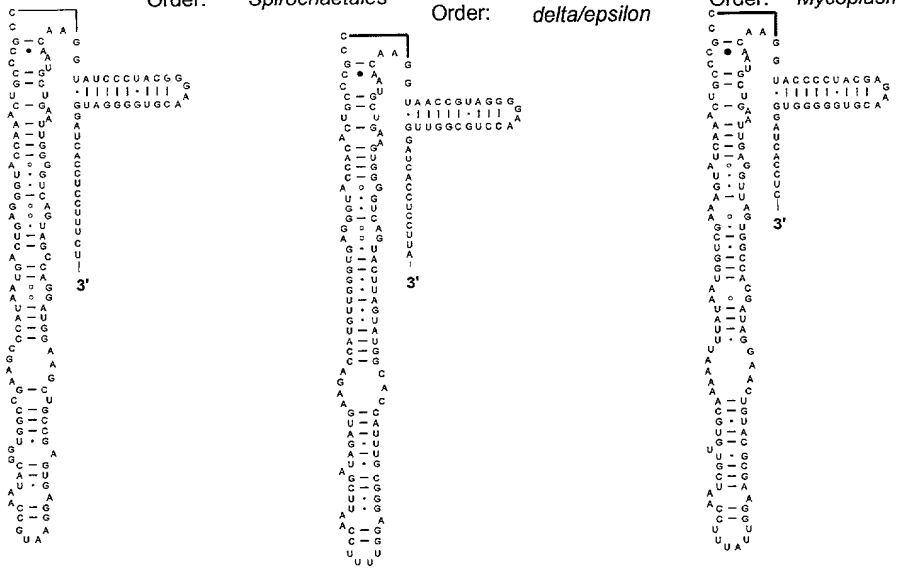
Domain: *Bacteria*
Kingdom:
Order: *Spirochaetales*

Campylobacter sputorum

Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *delta/epsilon*

Mycoplasma hyopneumoniae

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmales*



Clostridium innocuum

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmales*

Haemophilus influenzae

Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *gamma*

Mycoplasma genitalium

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmales*

Fig 11
The decoding site of 16SrRNA for range of bacteria

FIGURE 12

Secondary Structure: small subunit ribosomal RNA

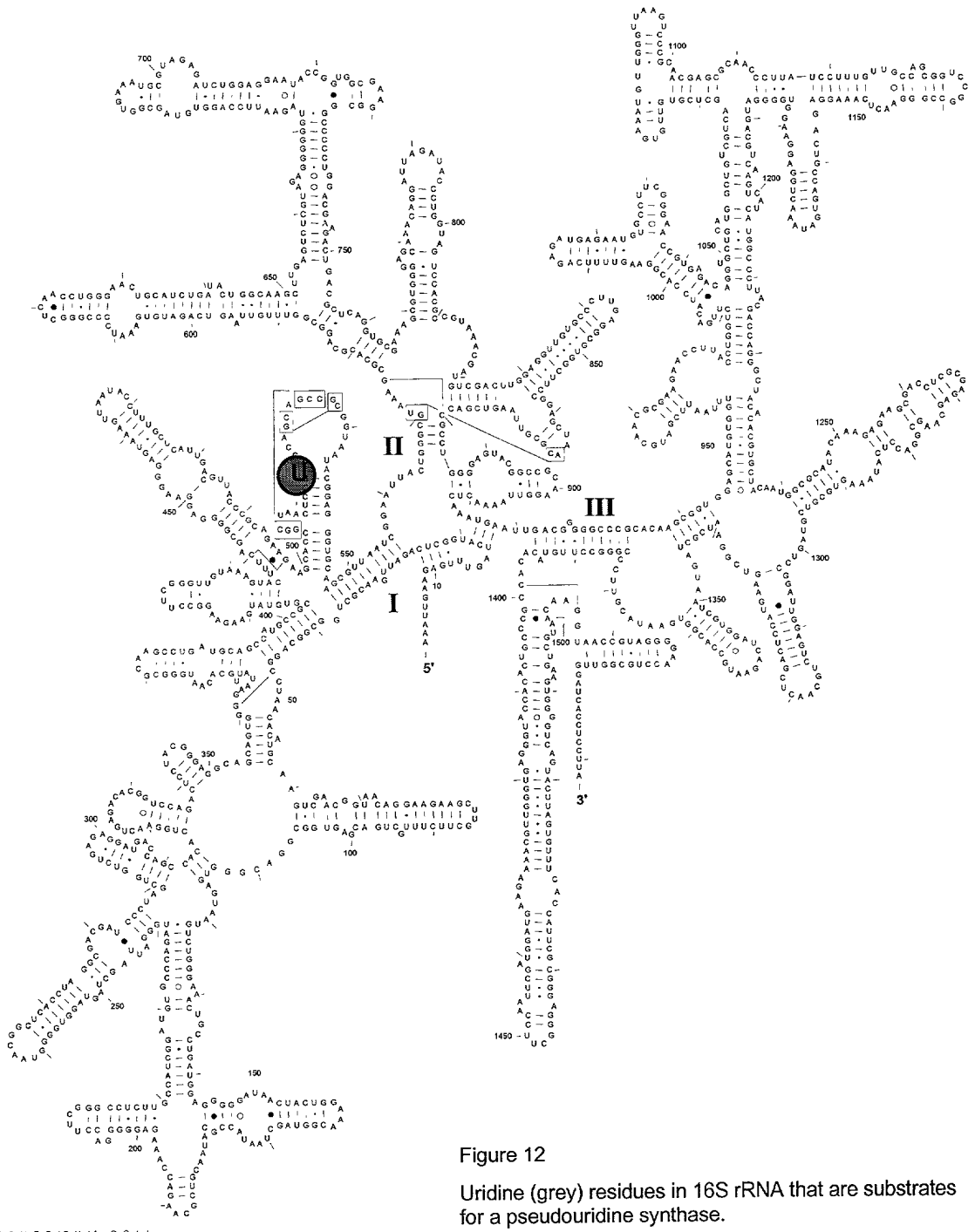


Figure 12

Uridine (grey) residues in 16S rRNA that are substrates for a pseudouridine synthase.

FIGURE 13

Secondary Structure: large subunit ribosomal RNA - 5' half

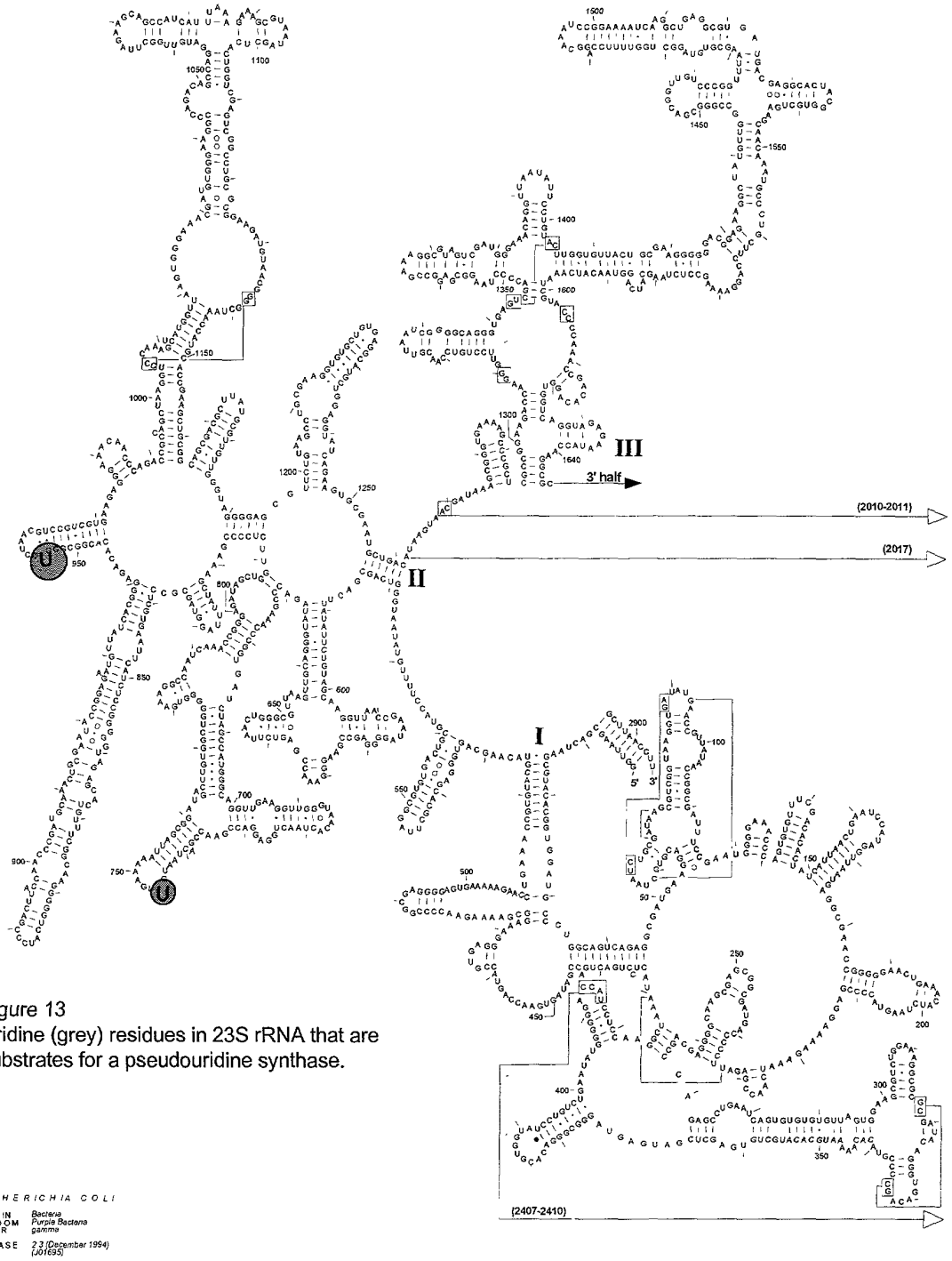


Figure 13
Uridine (grey) residues in 23S rRNA that are substrates for a pseudouridine synthase.

FIGURE 14

Secondary Structure: large subunit ribosomal RNA - 3' half

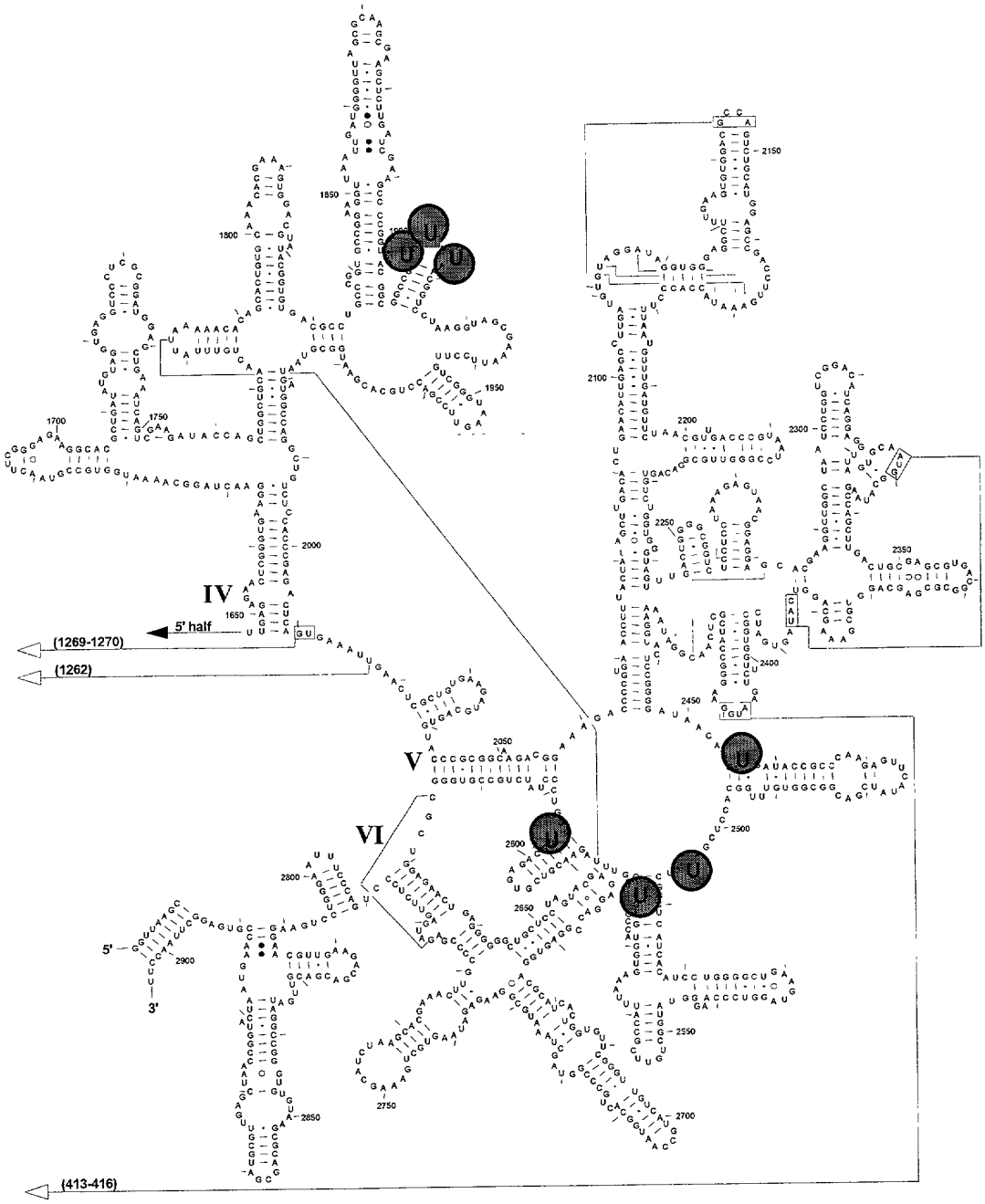


Figure 14

Uridine (grey) residues in 23S rRNA that are substrates for a pseudouridine synthase.

E S C H E R I C H I A C O L I

D O M A I N Bacteria
K I N G D O M Purple Bacteria
O R D E R gamma

R E L E A S E 2.3 (December 1994)
(J01695)

FIGURE 15

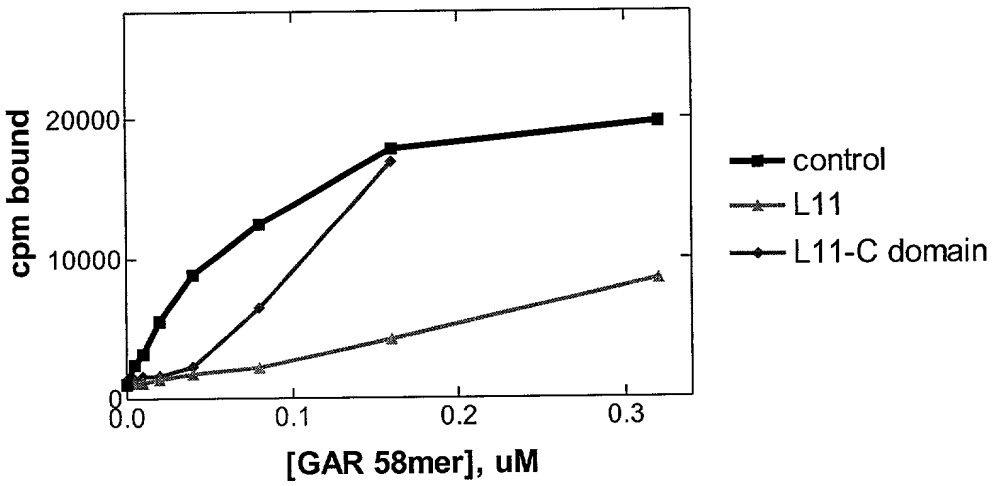
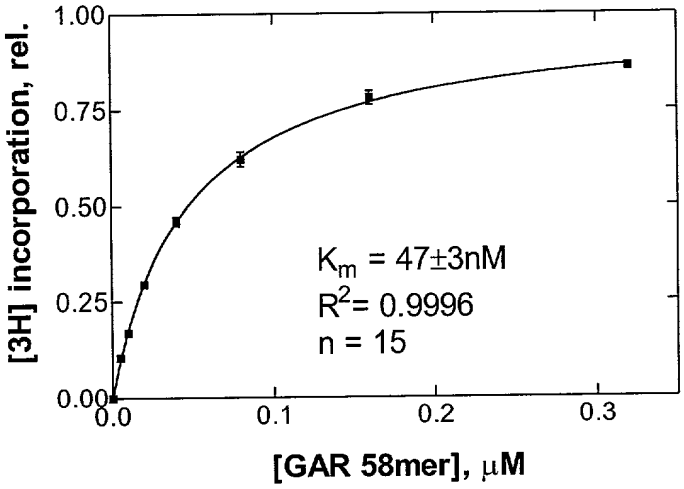


FIGURE 16

A


[3H] incorporation, rel.
1.00
0.75
0.50
0.25
0.00
0.0
0.1
0.2
0.3
K_m = 47±3nM
R^2= 0.9996
n = 15
[GAR 58mer], μM

B

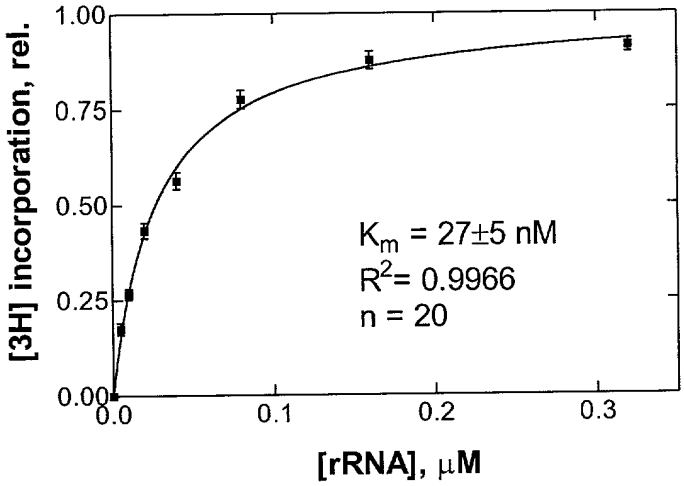

[3H] incorporation, rel.
1.00
0.75
0.50
0.25
0.00
0.0
0.1
0.2
0.3
K_m = 27±5 nM
R^2= 0.9966
n = 20
[rRNA], μM

FIGURE 17

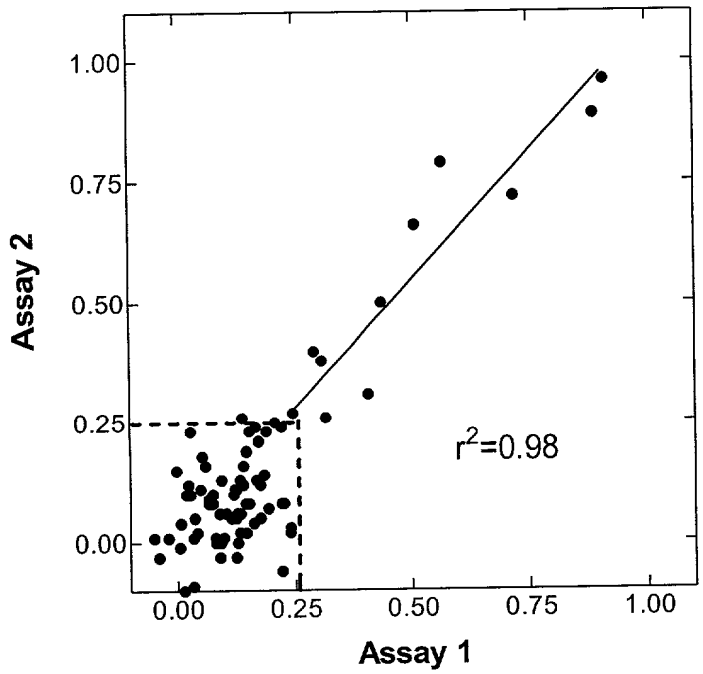


FIGURE 18

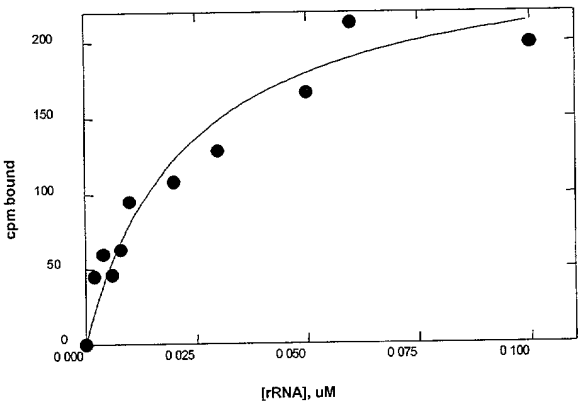


FIGURE 19

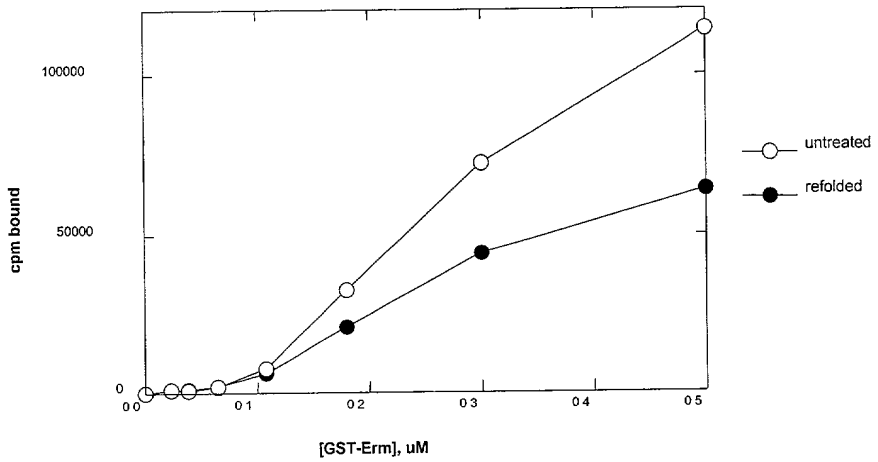


FIGURE 20

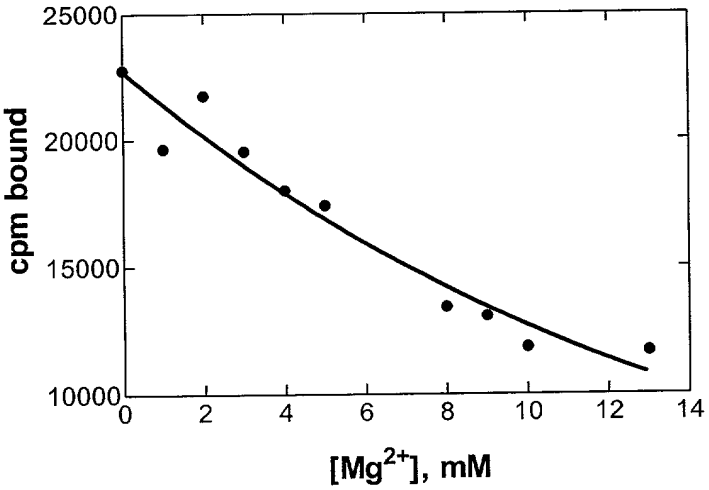


FIGURE 21

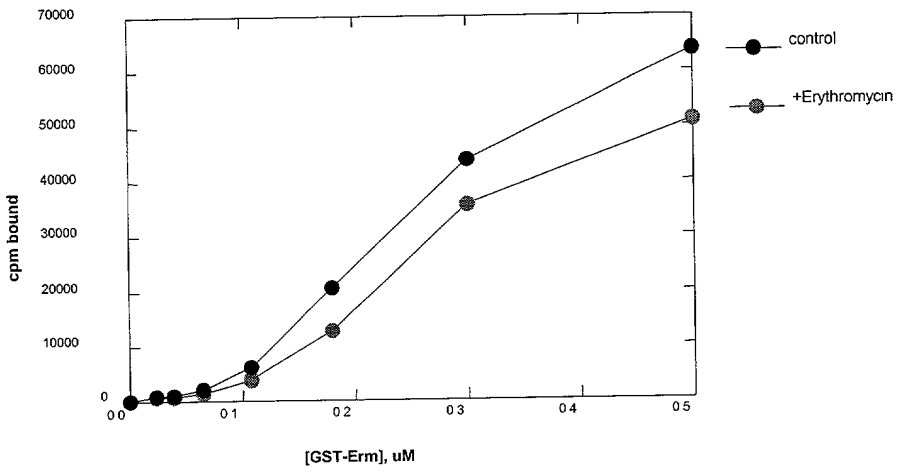
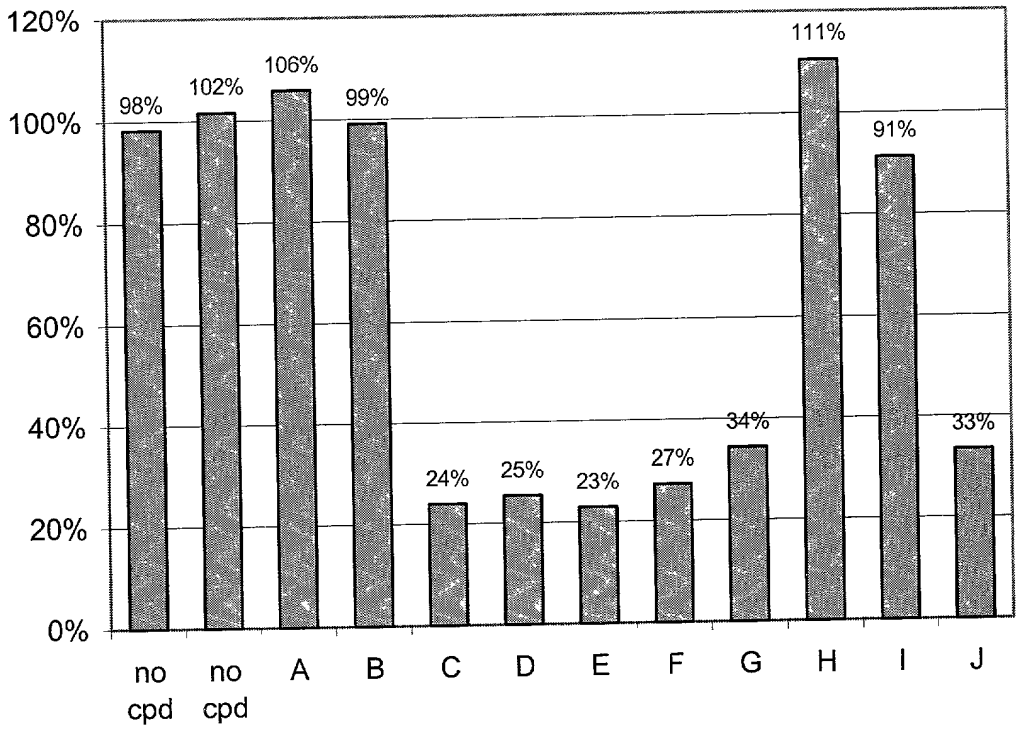


FIGURE 22


120%
100%
80%
60%
40%
20%
0%
98%
102%
106%
99%
24%
25%
23%
27%
34%
111%
91%
33%
no cpd
no cpd
A
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C
D
E
F
G
H
I
J